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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: (OTHER THAN US): THE UNIVERSITY OF MELBOURNE
(US ONLY): SINGH Mohan, BHALLA Prem, HUI-LING Xu and
SWOBODA Ines

(ii) TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
THEREFOR

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE
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(E) COUNTRY: AUSTRALIA
(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT INTERNATIONAL
(B) FILING DATE: 24-JUL-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO8233
(B) FILING DATE: 25-JUL-1997
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PP1184
(B) FILING DATE: 31-DEC-1997
(C) CLASSIFICATION:

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES, DR E JOHN L
(C) REFERENCE/DOCKET NUMBER: EJH/AF

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(ix) TELECOMMUNICATION INFORMATION:

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(C) TELEX: AA 31787

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTACTCTTAA GCATACAACA TGAG

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGGCATACT TGAATGCTAC AAGA

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 625 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 82..468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCATCCCAT CAACAGAAGG TTTAAGTGGA AATCCATTTT ATTAGAAAAG ATCGGACAAA	60
GGGTACTCTT AAGCATACAA C ATG AGG GCG GTG GCG GTT TTC TTT GCT TGC	111
Met Arg Ala Val Ala Val Phe Phe Ala Cys	
1 5 10	
GTT CTC TTC TGT ATG GTT CAC AAA GCC GCA CTT GCG GAT GAT AAA ACG	159
Val Leu Phe Cys Met Val His Lys Ala Ala Leu Ala Asp Asp Lys Thr	
15 20 25	
TGC AAC CCT ACA GAT TTT ATG GTT ACC CAA ACC ATA ACT GGA TTG ACA	207

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Ala	Val	Ala	Val	Phe	Phe	Ala	Cys	Val	Leu	Phe	Cys	Met	Val
1				5					10					15	
His	Lys	Ala	Ala	Leu	Ala	Asp	Asp	Lys	Thr	Cys	Asn	Pro	Thr	Asp	Phe
			20					25					30		
Met	Val	Thr	Gln	Thr	Ile	Thr	Gly	Leu	Thr	Ile	Gly	Gly	Lys	Gln	Glu
		35					40					45			
Phe	Glu	Val	Asn	Leu	Ile	Asn	Asn	Leu	Tyr	Cys	Ala	Gln	Ser	Asn	Val
	50					55					60				
Lys	Val	Ser	Cys	Asp	Gly	Leu	His	Thr	Thr	Glu	Pro	Ile	Asp	Pro	His
65					70					75					80
Ile	Ile	Arg	Pro	Leu	Ser	Asp	Gly	Thr	Asn	Asn	Cys	Leu	Val	Asn	Asn
				85					90					95	
Gly	Ala	Pro	Ile	Ser	His	Ala	Thr	Leu	Val	Ala	Phe	Lys	Tyr	Ala	Trp
			100					105					110		
Asp	Val	Pro	Pro	Ser	Phe	Ser	Ile	Ile	Ser	Ser	Asp	Ile	Asn	Cys	Ser OCH

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115

120

125

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 49..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5.

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GAAAGTTGAA ACATCTCCAT CAAACTCTAG AGTCAGATTT CCCACAAG ATG ATT TCA      57
                                   Met Ile Ser
                                   1

TCG GCA AAT AAC AAA GGC GCC GGC ACA AGC CGC CGC AAG CTC CGT TCT      105
Ser Ala Asn Asn Lys Gly Ala Gly Thr Ser Arg Arg Lys Leu Arg Ser
      5              10              15

GAG AAG GCT GCA CTC CAG TTC TCC GTC AGT CGC GTC GAA TAC TCC CTC      153
Glu Lys Ala Ala Leu Gln Phe Ser Val Ser Arg Val Glu Tyr Ser Leu
      20              25              30              35

AAG AAG GGG CGC TAT TGC AGG CGC TTA GGC GCT ACG GCC CCC GTC TAC      201
Lys Lys Gly Arg Tyr Cys Arg Arg Leu Gly Ala Thr Ala Pro Val Tyr
              40              45              50

CTA GCC GCC GTC CTT GAA AAC CTC GTG GCC GAA GTG TTG GAC ATG GCG      249
Leu Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu Asp Met Ala
              55              60              65

GCG AAC GTG ACA GAA GAA ACA TCC CCC ATT GTT ATC AAA CCG AGG CAT      297
Ala Asn Val Thr Glu Glu Thr Ser Pro Ile Val Ile Lys Pro Arg His
              70              75              80

ATT ATG CTT GCC CCC AGG AAT GAT GTA GAA GTT GAA CAA GCT GTT TCA      345
Ile Met Leu Ala Pro Arg Asn Asp Val Glu Val Glu Gln Ala Val Ser
              85              90              95

CGG TGT CAC CAT CTC GGC ATC AGG TGT CGT CCC TAAACACGC AAAGAGCTGG      398
Arg Cys His His Leu Gly Ile Arg Cys Arg Pro
      100              105              110

ACCGTCGCAA ACGCCGTTCC ACCTTTCAGC CGGATTAGTT CTTGATATTT CATTCTATCA      458

ATCTTGTTTA TGTGACTGTG ATTTTTCGTT TTGTGTTGAA CTAAGCCCCC TAATCTGGAT      518

TTCTCGTTTT ATGTTGAACT AAGTCTGTGC ACTCTTGAAG TAAAAAAAAA AAAAAAAAAA      578
AAAAAAAAAA
                                   587
  
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(2) INFORMATION FOR SEQ ID NO:6:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Ile Ser Ser Ala Asn Asn Lys Gly Ala Gly Thr Ser Arg Arg Lys
 1           5           10           15
Leu Arg Ser Glu Lys Ala Ala Leu Gln Phe Ser Val Ser Arg Val Glu
          20           25           30
Tyr Ser Leu Lys Lys Gly Arg Tyr Cys Arg Arg Leu Gly Ala Thr Ala
          35           40           45
Pro Val Tyr Leu Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu
          50           55           60
Asp Met Ala Ala Asn Val Thr Glu Glu Thr Ser Pro Ile Val Ile Lys
 65           70           75           80
Pro Arg His Ile Met Leu Ala Pro Arg Asn Asp Val Glu Val Glu Gln
          85           90           95
Ala Val Ser Arg Cys His His Leu Gly Ile Arg Cys Arg Pro
          100          105          110

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 16..348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GATCCCAAAT CATCA ATG ACG ATC CCC GAA AAG AAA TCC GTC GCT CCG ATG      51
      Met Thr Ile Pro Glu Lys Lys Ser Val Ala Pro Met
              1              5              10
GCC CGT ATG AAG CAT ACA GCC CGC ATG TCT ACC GGC GGT AAG GCT CCA      99
Ala Arg Met Lys His Thr Ala Arg Met Ser Thr Gly Gly Lys Ala Pro
          15          20          25
CGC AAG CAG CTC GCC TCT AAG GCT CTT CGC AAG GCG CCA CCA CCA CCG      147
Arg Lys Gln Leu Ala Ser Lys Ala Leu Arg Lys Ala Pro Pro Pro Pro
          30          35          40
ACC AAA GGA GTG AAG CAG CCC ACC ACT ACC ACC TCC GGA AAA TGG CGC      195
Thr Lys Gly Val Lys Gln Pro Thr Thr Thr Thr Ser Gly Lys Trp Arg
          45          50          55          60
TTC GCG AGA TTT CAC AGG AAA CTG CCA TTC CAA GGG CTG GTG AGG AAA      243
Phe Ala Arg Phe His Arg Lys Leu Pro Phe Gln Gly Leu Val Arg Lys
          65          70          75

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ATC TGG CAG GAC TTG AAG ACA CAT CTG CGC TTC AAG AAC CAC TCG GTT	291
Ile Trp Gln Asp Leu Lys Thr His Leu Arg Phe Lys Asn His Ser Val	
80 85 90	
CCT CCA CTT GAG GAG GTA ACT GAG GTT TAT CCT TGC CAA ACT ATT GGA	339
Pro Pro Leu Glu Glu Val Thr Glu Val Tyr Pro Cys Gln Thr Ile Gly	
95 100 105	
GGA TGC TAT TAGGATATTG AATTGGATA ATGGTTTAAT TATCTGTTCT	388
Gly Cys Tyr	
110	
ACCTTTATGA TCAAATTTCT GTGGCTCAGC GTTGTGTAAT TTGGGCAATC GAATTCTTAG	448
CTATATTGCC TCAAAAAAAAA AAAAAAAAAA AAAAAAA	485

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ile Pro Glu Lys Lys Ser Val Ala Pro Met Ala Arg Met Lys	
1 5 10 15	
His Thr Ala Arg Met Ser Thr Gly Gly Lys Ala Pro Arg Lys Gln Leu	
20 25 30	
Ala Ser Lys Ala Leu Arg Lys Ala Pro Pro Pro Pro Thr Lys Gly Val	
35 40 45	
Lys Gln Pro Thr Thr Thr Thr Ser Gly Lys Trp Arg Phe Ala Arg Phe	
50 55 60	
His Arg Lys Leu Pro Phe Gln Gly Leu Val Arg Lys Ile Trp Gln Asp	
65 70 75 80	
Leu Lys Thr His Leu Arg Phe Lys Asn His Ser Val Pro Pro Leu Glu	
85 90 95	
Glu Val Thr Glu Val Tyr Pro Cys Gln Thr Ile Gly Gly Cys Tyr	
100 105 110	

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAGGGTGTGTT GGAATTAGGT TTGCCTAGGG TTTGCCTAGG TTTAGAGAAA TAGTCAAAAT 60
TGTCCTATTC TATAGGCATG ATTTAGTAGT GAGTTAATTA TCCTATAATT TCTCTTCTTG 120
TATGCTCAAA TAACTGGTTC TTAAATGAAT AGATAATTAA GTTTTGTAGC AATTTCTTCC 180
TCAAATTGAG TATCAACAAT TGTTAGATTG CTTTGGTGAT TATATTTGAT ATAATTGTTT 240
GTAAGAATGT GTAGTGAAAA GATTGTGATT ATTCATTTCC TTGTTGGACG AATTGTTAGA 300
GCCCCATCGC TAATGCCTTA TAGTACTCGA AATATGTTGG GAATAGAAGA TGAAAAATCC 360
CATTCTTTGT AGTAGGAGTA AAAATTTGTC TTTTCATTAT TCCATTGAAT GTTAACCACT 420
TGCCATTCAT CTGACGGGGA TGGCAGAGTT CCGACCATCT AGTGATCCGT GGGATATTGA 480
TTTTGGTGTG TCAATGAAAT TGTGAGAACG GGCTTCTGGG AGAGAAAAGC CCTCTTGCCT 540
CTGATATGAA CACTGAGGCT GATTATGTGA ACGGATGGAG ATTTATCAGT GGCTGAATTT 600
GGGTGCTGTA GAGACAGAAT TTGAAAGTTC TAACAATAAA CCCTAATTCT GAACTTGGGC 660
GGGGCTGGGA TTTTACTCTT AACGTGAAGA GAGGCAAGAT GAATTGACAG CTTGGAAGTC 720
GATCCAGTAT TTGCAGCAGT CGTGACGAAT TGGTTGGACA GTTACATCGG TCAGAGAATG 780
CGTTCTATAA ATTCCCCCAA TGCGGCAGTG AAAATCCCAT CCCATCAACA GAAGTTTTAA 840
GTGGAAACCC ATTCCAATAG AGAAGATCGA ACAAAGGGTA TTAAACATA CAAATGGGGG 900
CAGTGGTGTG TCTTTTGTCT TGCGTTCTCT TCTGTATGGT TCACA 945

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGCATACT TGAATGCTAC AAGA

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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGTGAACCAT ACAGAAGAGA ACGC

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